

We present, JAZZ, a new graphical algorithm for whole genome assembly that self-consistently treats paired-end constraints. The algorithm is designed to be scalable for application to large animal and plant genome sequencing projects. To aid in the development and validation of assemblies, we have also developed a suite of graphical tools for examining and manipulating large layouts. JAZZ has been used at the JGI to put together then genomes of many microbes, a fungal genome, and the genomes of two chordates, the sea squirt *Ciona intestinalis* and the puffer fish *Fugu ruripes*; long, highly accurate scaffolds are recovered that are excellent substrates for annotation. We discuss the challenges faced in assembling these genomes, and strategies for future sequencing projects.